

RAW SEQUENCE LISTING

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Application Serial Number: 10/595,858
Source: IFWO
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RAW SEQUENCE LISTING

DATE: 06/02/2006

PATENT APPLICATION: US/10/595,858

TIME: 09:22:00

Input Set : A:\Sequence Listing to File.TXT

Output Set: N:\CRF4\06022006\J595858.raw

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3 <110> APPLICANT: YOSHINAGA, Takashi
4   ARAI, Toru
6 <120> TITLE OF INVENTION: hERG channel-expressing cell
8 <130> FILE REFERENCE: 09857/0204372-US0
10 <140> CURRENT APPLICATION NUMBER: 10/595,858
11 <141> CURRENT FILING DATE: 2006-05-16
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/017441
14 <151> PRIOR FILING DATE: 2004-11-17
16 <150> PRIOR APPLICATION NUMBER: JP 2003-387255
17 <151> PRIOR FILING DATE: 2003-11-17
19 <160> NUMBER OF SEQ ID NOS: 13
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4070
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo Sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (184)..(3660)
33 <400> SEQUENCE: 1
34 acgcggcctg ctcaggcctc cagcggcccg tgcggaggga ggcgggaggc gagcgaggac      60
36 ccgcgcccgc agtccagtct gtgcgcgcc gtgctcgctt ggcgcggtgc gggaccagcg      120
38 ccggccaccc gaagcctagt gcgtcgcccg gtgggtgggc ccgcccggcg ccatgggctc      180
40 agg atg ccg gtg cgg agg ggc cac gtc gcg ccg cag aac acc ttc ctg      228
41   Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu
42   1          5          10          15
44 gac acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc      276
45 Asp Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile
46          20          25          30
48 gcc aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc      324
49 Ala Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly
50          35          40          45
52 ttc tgc gag ctg tgc ggc tac tcg cgg gcc gag gtg atg cag cga ccc      372
53 Phe Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro
54          50          55          60
56 tgc acc tgc gac ttc ctg cac ggg ccg cgc acg cag cgc cgc gct gcc      420
57 Cys Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala
58          65          70          75
60 gcg cag atc gcg cag gca ctg ctg ggc gcc gag gag cgc aaa gtg gaa      468
61 Ala Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu
62 80          85          90          95
64 atc gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat      516
65 Ile Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp

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66	100	105	110	
68	gtg gtg ccc gtg aag aac gag gat ggg gct gtc atc atg ttc atc ctc	564		
69	Val Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu			
70	115 120 125			
72	aat ttc gag gtg gtg atg gag aag gac atg gtg ggg tcc ccg gct cat	612		
73	Asn Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His			
74	130 135 140			
76	gac acc aac cac cgg ggc ccc ccc acc agc tgg ctg gcc cca ggc cgc	660		
77	Asp Thr Asn His Arg Gly Pro Thr Ser Trp Leu Ala Pro Gly Arg			
78	145 150 155			
80	gcc aag acc ttc cgc ctg aag ctg ccc gcg ctg ctg gcg ctg acg gcc	708		
81	Ala Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala			
82	160 165 170 175			
84	cgg gag tcg tcg gtg cgg tcg ggc ggc gcg ggc ggc gcg ggc gcc ccg	756		
85	Arg Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro			
86	180 185 190			
88	ggg gcc gtg gtg gtg gac gtg gac ctg acg ccc gcg gca ccc agc agc	804		
89	Gly Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser			
90	195 200 205			
92	gag tcg ctg gcc ctg gac gaa gtg aca gcc atg gac aac cac gtg gca	852		
93	Glu Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala			
94	210 215 220			
96	ggg ctc ggg ccc gcg gag gag cgg cgt gcg ctg gtg ggt ccc ggc tct	900		
97	Gly Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser			
98	225 230 235			
100	ccg ccc cgc agc gcg ccc ggc cag ctc cca tcg ccc cgg gcg cac agc	948		
101	Pro Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser			
102	240 245 250 255			
104	ctc aac ccc gac gcc tcg ggc tcc agc tgc agc ctg gcc cgg acg cgc	996		
105	Leu Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg			
106	260 265 270			
108	tcc cga gaa agc tgc gcc agc gtg cgc cgc gcc tcg tcg gcc gac gac	1044		
109	Ser Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp			
110	275 280 285			
112	atc gag gcc atg cgc gcc ggg gtg ctg ccc ccg cca ccg cgc cac gcc	1092		
113	Ile Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala			
114	290 295 300			
116	agc acc ggg gcc atg cac cca ctg cgc agc ggc ttg ctc aac tcc acc	1140		
117	Ser Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr			
118	305 310 315			
120	tcg gac tcc gac ctc gtg cgc tac cgc acc att agc aag att ccc caa	1188		
121	Ser Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln			
122	320 325 330 335			
124	atc acc ctc aac ttt gtg gac ctc aag ggc gac ccc ttc ttg gct tcg	1236		
125	Ile Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser			
126	340 345 350			
128	ccc acc agt gac cgt gag atc ata gca cct aag ata aag gag cga acc	1284		
129	Pro Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr			
130	355 360 365			

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132 cac aat gtc act gag aag gtc acc cag gtc ctg tcc ctg ggc gcc gac 1332
133 His Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp
134      370      375      380
136 gtg ctg cct gag tac aag ctg cag gca ccg cgc atc cac cgc tgg acc 1380
137 Val Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr
138      385      390      395
140 atc ctg cat tac agc ccc ttc aag gcc gtg tgg gac tgg ctc atc ctg 1428
141 Ile Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu
142 400      405      410      415
144 ctg ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc ttc 1476
145 Leu Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe
146      420      425      430
148 ctg ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc tac 1524
149 Leu Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr
150      435      440      445
152 gcc tgc cag ccg ctg gct gtg gtg gac ctc atc gtg gac atc atg ttc 1572
153 Ala Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe
154      450      455      460
156 att gtc gac atc ctc atc aac ttc cgc acc acc tac gtc aat gcc aac 1620
157 Ile Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn
158      465      470      475
160 gag gag gtg gtc agc cac ccc ggc cgc atc gcc gtc cac tac ttc aag 1668
161 Glu Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys
162 480      485      490      495
164 ggc tgg ttc ctc atc gac atg gtg gcc gcc atc ccc ttc gac ctg ctc 1716
165 Gly Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu
166      500      505      510
168 atc ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act gcg 1764
169 Ile Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala
170      515      520      525
172 cgg ctg ctg cgg ctg gtg cgc gtg gcg cgg aag ctg gat cgc tac tca 1812
173 Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser
174      530      535      540
176 gag tac ggc gcg gcc gtg ctg ttc ttg ctc atg tgc acc ttt gcg ctc 1860
177 Glu Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu
178      545      550      555
180 atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg gag 1908
181 Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu
182 560      565      570      575
184 cag cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc gac 1956
185 Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp
186      580      585      590
188 cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc atc 2004
189 Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile
190      595      600      605
192 aag gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc acc 2052
193 Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr
194      610      615      620
196 agt gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag atc 2100

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197	Ser	Val	Gly	Phe	Gly	Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Ile	
198		625					630					635					
200	ttc	tcc	atc	tgc	gtc	atg	ctc	att	ggc	tcc	ctc	atg	tat	gct	agc	atc	2148
201	Phe	Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	
202	640					645					650					655	
204	ttc	ggc	aac	gtg	tcg	gcc	atc	atc	cag	cgg	ctg	tac	tcg	ggc	aca	gcc	2196
205	Phe	Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	
206					660					665						670	
208	cgc	tac	cac	aca	cag	atg	ctg	cgg	gtg	cgg	gag	ttc	atc	cgc	ttc	cac	2244
209	Arg	Tyr	His	Thr	Gln	Met	Leu	Arg	Val	Arg	Glu	Phe	Ile	Arg	Phe	His	
210				675					680					685			
212	cag	atc	ccc	aat	ccc	ctg	cgc	cag	cgc	ctc	gag	gag	tac	ttc	cag	cac	2292
213	Gln	Ile	Pro	Asn	Pro	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	
214			690					695					700				
216	gcc	tgg	tcc	tac	acc	aac	ggc	atc	gac	atg	aac	gcg	gtg	ctg	aag	ggc	2340
217	Ala	Trp	Ser	Tyr	Thr	Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	
218		705					710					715					
220	ttc	cct	gag	tgc	ctg	cag	gct	gac	atc	tgc	ctg	cac	ctg	aac	cgc	tca	2388
221	Phe	Pro	Glu	Cys	Leu	Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	Asn	Arg	Ser	
222	720					725					730				735		
224	ctg	ctg	cag	cac	tgc	aaa	ccc	ttc	cga	ggg	gcc	acc	aag	ggc	tgc	ctt	2436
225	Leu	Leu	Gln	His	Cys	Lys	Pro	Phe	Arg	Gly	Ala	Thr	Lys	Gly	Cys	Leu	
226				740					745					750			
228	cgg	gcc	ctg	gcc	atg	aag	ttc	aag	acc	aca	cat	gca	ccg	cca	ggg	gac	2484
229	Arg	Ala	Leu	Ala	Met	Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	
230				755					760					765			
232	aca	ctg	gtg	cat	gct	ggg	gac	ctg	ctc	acc	gcc	ctg	tac	ttc	atc	tcc	2532
233	Thr	Leu	Val	His	Ala	Gly	Asp	Leu	Leu	Thr	Ala	Leu	Tyr	Phe	Ile	Ser	
234			770					775					780				
236	cgg	ggc	tcc	atc	gag	atc	ctg	cgg	ggc	gac	gtc	gtc	gtg	gcc	atc	ctg	2580
237	Arg	Gly	Ser	Ile	Glu	Ile	Leu	Arg	Gly	Asp	Val	Val	Val	Ala	Ile	Leu	
238		785					790					795					
240	ggg	aag	aat	gac	atc	ttt	ggg	gag	cct	ctg	aac	ctg	tat	gca	agg	cct	2628
241	Gly	Lys	Asn	Asp	Ile	Phe	Gly	Glu	Pro	Leu	Asn	Leu	Tyr	Ala	Arg	Pro	
242	800					805					810				815		
244	ggc	aag	tcg	aac	ggg	gat	gtg	cgg	gcc	ctc	acc	tac	tgt	gac	cta	cac	2676
245	Gly	Lys	Ser	Asn	Gly	Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	
246				820					825					830			
248	aag	atc	cat	cgg	gac	gac	ctg	ctg	gag	gtg	ctg	gac	atg	tac	cct	gag	2724
249	Lys	Ile	His	Arg	Asp	Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Glu	
250				835					840					845			
252	ttc	tcc	gac	cac	ttc	tgg	tcc	agc	ctg	gag	atc	acc	ttc	aac	ctg	cga	2772
253	Phe	Ser	Asp	His	Phe	Trp	Ser	Ser	Leu	Glu	Ile	Thr	Phe	Asn	Leu	Arg	
254			850					855					860				
256	gat	acc	aac	atg	atc	ccg	ggc	tcc	ccc	ggc	agt	acg	gag	tta	gag	ggc	2820
257	Asp	Thr	Asn	Met	Ile	Pro	Gly	Ser	Pro	Gly	Ser	Thr	Glu	Leu	Glu	Gly	
258		865					870					875					
260	ggc	ttc	agt	cgg	caa	cgc	aag	cgc	aag	ttg	tcc	ttc	cgc	agg	cgc	acg	2868
261	Gly	Phe	Ser	Arg	Gln	Arg	Lys	Arg	Lys	Leu	Ser	Phe	Arg	Arg	Arg	Thr	

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262	880		885		890		895	
264	gac aag gac acg gag cag cca ggg gag gtg tgc gcc ttg ggg ccg ggc	2916						
265	Asp Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly							
266			900		905		910	
268	cgg gcg ggg gca ggg ccg agt agc cgg ggc cgg ccg ggg ggg ccg tgg	2964						
269	Arg Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp							
270			915		920		925	
272	ggg gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag gat	3012						
273	Gly Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp							
274			930		935		940	
276	gag ggc cca ggc cgc agc tcc agc ccc ctc cgc ctg gtg ccc ttc tcc	3060						
277	Glu Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser							
278			945		950		955	
280	agc ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg gag	3108						
281	Ser Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu							
282	960		965		970		975	
284	gac tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc ttc	3156						
285	Asp Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe							
286			980		985		990	
288	tca gga gtg tcc aac att ttc agc ttc tgg ggg gac agt cgg ggc cgc	3204						
289	Ser Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg							
290			995		1000		1005	
292	cag tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc	3249						
293	Gln Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu							
294			1010		1015		1020	
296	ctc aac atc ccc ctc tcc agc ccg ggt cgg cgg ccc cgg ggc gac	3294						
297	Leu Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp							
298			1025		1030		1035	
300	gtg gag agc agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg	3339						
301	Val Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu							
302			1040		1045		1050	
304	gag acc cgg ctg agt gca gac atg gcc act gtc ctg cag ctg cta	3384						
305	Glu Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu							
306			1055		1060		1065	
308	cag agg cag atg acg ctg gtc ccg ccc gcc tac agt gct gtg acc	3429						
309	Gln Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr							
310			1070		1075		1080	
312	acc ccg ggg cct ggc ccc act tcc aca tcc ccg ctg ttg ccc gtc	3474						
313	Thr Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val							
314			1085		1090		1095	
316	agc ccc ctc ccc acc ctc acc ttg gac tgc ctt tct cag gtt tcc	3519						
317	Ser Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser							
318			1100		1105		1110	
320	cag ttc atg gcg tgt gag gag ctg ccc ccg ggg gcc cca gag ctt	3564						
321	Gln Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu							
322			1115		1120		1125	
324	ccc caa gaa ggc ccc aca cga cgc ctc tcc cta ccg ggc cag ctg	3609						
325	Pro Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu							
326			1130		1135		1140	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12

VERIFICATION SUMMARY

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